



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Goeddel, David V. Rothe. Mike
- (ii) TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
- (iii) NUMBER OF SEQUENCES: 59

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 460 Point San Bruno Blvd
- (C) CITY: South San Francisco
- (D) STATE: California(E) COUNTRY: USA
- (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 07-Jan-1997
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Dreger, Ginger R.
- (B) REGISTRATION NUMBER: 33,055
- (C) REFERENCE/DOCKET NUMBER: P0897C2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415/225-3216
- (B) TELEFAX: 415/952-9881
- (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2088 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCAGCCGG TTCTCTGCCC CAAGGACGCT ACCGCCCAAT GCGAGCAGAA 50 GGCGGCGCAC AGATACAGAA AGTGAGGCTC AGACATATTG AAGACCGTGT 100 GACATAGGGT AGCCAAATGA CAGTGTGAGA AAGTGACATT TACTCAAGGC 150 CACCCAGATA TCCTGGAGGA CCCAGAACCC TGGAGATTCC CATCAGAAAG 200 ACCTTCTGGC CACCTGAAAC CCCAAGATGG CCTCCAGCTC AGCCCCTGAT 250 GAAAACGAGT TTCAATTTGG TTGCCCCCCT GCTCCCTGCC AGGACCCATC 300 GGAGCCCAGA GTTCTCTGCT GCACAGCCTG TCTCTCTGAG AACCTGAGAG 350 ATGATGAGGA TCGGATCTGT CCTAAATGCA GAGCAGACAA CCTCCATCCT 400 GTGAGCCCAG GAAGCCCTCT GACTCAGGAG AAGGTTCACT CTGATGTAGC 450 TGAGGCTGAA ATCATGTGCC CCTTTGCAGG TGTTGGCTGT TCCTTCAAGG 500 GGAGCCCACA ATCCATGCAG GAGCATGAGG CTACCTCCCA GTCCTCCCAC 550 CTGTACCTGC TGCTGGCGGT CTTAAAGGAG TGGAAATCCT CACCAGGCTC 600 CAACCTAGGG TCTGCACCCA TGGCACTGGA GCGGAACCTG TCAGAGCTGC 650 AGCTTCAGGC AGCTGTGGAA GCGACAGGGG ACCTGGAGGT AGACTGCTAC 700 CGGGCACCTT GCTGTGAGAG CCAGGAAGAA CTGGCCCTGC AGCACTTGGT 750 GAAGGAGAAG CTGCTGGCTC AGCTGGAGGA GAAGCTGCGT GTGTTTGCAA 800

ACATTGTTGC TGTCCTCAAC AAGGAAGTGG AGGCTTCCCA CCTGGCACTG 850 GCCGCCTCCA TCCACCAGAG CCAGTTGGAC CGAGAGCACC TCCTGAGCTT 900 GGAGCAGAGG GTGGTGGAAT TACAGCAAAC CCTGGCTCAA AAAGACCAGG 950 TCCTGGGCAA GCTTGAGCAC AGTCTGCGAC TCATGGAGGA GGCATCCTTT 1000 GATGGTACTT TCCTGTGGAA GATCACCAAT GTCACCAAGC GGTGCCACGA 1050 GTCAGTGTGT GGCCGGACTG TCAGCCTCTT CTCTCCAGCT TTCTACACTG 1100 CCAAGTATGG TTACAAGTTG TGCCTGCGCT TGTACCTGAA CGGGGATGGC 1150 TCAGGCAAGA AGACCCACCT GTCCCTCTTC ATCGTGATCA TGAGAGGAGA 1200 ATACGATGCT CTCCTGCCCT GGCCTTTCAG GAACAAGGTC ACCTTTATGC 1250 TACTTGACCA GAACAACCGA GAGCATGCTA TTGATGCCTT CCGGCCTGAC 1300 CTGAGCTCAG CCTCCTTCCA GCGGCCACAG AGTGAGACCA ACGTGGCCAG 1350 CGGCTGCCCG CTCTTCTTCC CCCTCAGCAA GCTGCAGTCA CCCAAGCACG 1400 CCTACGTCAA AGATGACACA ATGTTCCTCA AATGCATTGT GGACACTAGT 1450 GCTTAGGGAT GGGGGGAGGG GGTGTCTCCT GACAGAACCA GCTTAGACTG 1500 GGGGACTTAG CTAGACAGCC AGGCCCTGCC TGCCCTTGGA GCCCACAGCC 1550 CACGACAAGG AGGAGCCAAG GCTGGCATGA CTTCAGCGCC ACAGCATGCT 1600 GGTTATGGCT GATGTGAGGC TGGAGAAACG TGTGCGTACA GAGACAGAGT 1650 GGAGGAGAAG ACAGAAGTGC TCTTTTCACA CAGACTACAC GACACCAGGA 1700 GGCCAGCATG CCAGCAGCTT CTGAATGTTG AGACCAGCCT AGATCAGGAT 1750 GAAAAGAGCC AGGCCTGAGG CTTGGACATT GAGCCAAGGC TATGGGGCCT 1800 AAGTGGAGGG GCACTCCTAC CAGGACATTC TCTCGAGGTC AGGGCATAAC 1850



TGGAAAAATG CCCCCATCTC TCTGTTCAGA CTCAAAACTA GAACCACAGG 1900
GCAGAAGGGT CAGACATTAA TGTGAATTTA ACCTGCCCTG GACTGAGTTC 1950
CTATGTTAAC AGACACGCAA ACAGGTAAAC CCAGAAACTG CCCTGGGAAA 2000
TGCTTTCTGG CTGCATCTGG AGATCTTTGA TGTTTTTACC GACAAAACAA 2050
ATAACAAAAG CCTTGAATTG CAAAAAAAAA AAAAAAAA 2088

- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Ser Ser Ala Pro Asp Glu Asn Glu Phe Gln Phe Gly

l 5

10

15

Cys Pro Pro Ala Pro Cys Gln Asp Pro Ser Glu Pro Arg Val Leu

20

25

30

Cys Cys Thr Ala Cys Leu Ser Glu Asn Leu Arg Asp Asp Glu Asp

35

40

45

Arg Ile Cys Pro Lys Cys Arg Ala Asp Asn Leu His Pro Val Ser

50

55

60

Pro Gly Ser Pro Leu Thr Gln Glu Lys Val His Ser Asp Val Ala

65

70

75

Glu Ala Glu Ile Met Cys Pro Phe Ala Gly Val Gly Cys Ser Phe

80

85

90

Lys Gly Ser Pro Gln Ser Met Gln Glu His Glu Ala Thr Ser Gln

95

100

105



| Ser Ser His Let | ı Tyr Leu Leu Leı | u Ala Val Leu Lys Glu 1 | Trp Lys |
|-----------------|--------------------------|--------------------------------|---------|
| 110 | 115 | 120 | |
| Ser Ser Pro Gly | Ser Asn Leu Gly | Ser Ala Pro Met Ala Lo | eu Glu |
| 125 | 130 | 135 | |
| Arg Asn Leu So | er Glu Leu Gln Le 145 | eu Gln Ala Ala Val Glu 150 | Ala Thr |
| Gly Asp Leu G | lu Val Asp Cys T | yr Arg Ala Pro Cys Cys | Glu Ser |
| 155 | 160 | 165 | |
| Gln Glu Glu Le | eu Ala Leu Gln Hi | is Leu Val Lys Glu Lys | Leu Leu |
| 170 | 175 | 180 | |
| Ala Gln Leu Gl | u Glu Lys Leu Ai | rg Val Phe Ala Asn Ile V | /al Ala |
| 185 | 190 | 195 | |
| Val Leu Asn Ly | ys Glu Val Glu Al | la Ser His Leu Ala Leu A | Ala Ala |
| 200 | 205 | 210 | |
| Ser Ile His Gln | Ser Gln Leu Asp | Arg Glu His Leu Leu Se | er Leu |
| 215 | 220 | 225 | |
| Glu Gln Arg Va | al Val Glu Leu Gl | n Gln Thr Leu Ala Gln 2 | Lys Asp |
| 230 | 235 | 240 | |
| Gln Val Leu Gl | y Lys Leu Glu Hi | is Ser Leu Arg Leu Met | Glu Glu |
| 245 | 250 | 255 | |
| Ala Ser Phe As | p Gly Thr Phe Le | u Trp Lys Ile Thr Asn V | al Thr |
| 260 | 265 | 270 | |
| Lys Arg Cys Hi | is Glu Ser Val Cy | s Gly Arg Thr Val Ser L | eu Phe |
| 275 | 280 | 285 | |
| Ser Pro Ala Phe | e Tyr Thr Ala Lys | Tyr Gly Tyr Lys Leu C | ys Leu |
| 290 | 295 | 300 | |
| Arg Leu Tyr Le | eu Asn Gly Asp G 310 | ely Ser Gly Lys Lys Thr 315 | His Leu |

Ser Leu Phe Ile Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu 320 325 330

Pro Trp Pro Phe Arg Asn Lys Val Thr Phe Met Leu Leu Asp Gln 335 340 345

Asn Asn Arg Glu His Ala Ile Asp Ala Phe Arg Pro Asp Leu Ser 350 355 360

Ser Ala Ser Phe Gln Arg Pro Gln Ser Glu Thr Asn Val Ala Ser 365 370 375

Gly Cys Pro Leu Phe Phe Pro Leu Ser Lys Leu Gln Ser Pro Lys 380 385 390

His Ala Tyr Val Lys Asp Asp Thr Met Phe Leu Lys Cys Ile Val 395 400 405

Asp Thr Ser Ala
409

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2121 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGCGAAGAC CGTTGGGGCT TTGTGGTGTG TGGGGGTTGT AACTCACATG 50
GCTGCAGCCA GTGTGACTTC CCCTGGCTCC CTAGAACTGC TACAGCCTGG 100
CTTCTCCAAG ACCCTCCTGG GGACCAGGTT AGAAGCCAAG TACCTCTGTT 150
CAGCCTGCAA AAACATCCTG CGGAGGCCTT TCCAGGCCCA GTGTGGGCAC 200
CGCTACTGCT CCTTCTGCCT GACCAGCATC CTCAGCTCTG GGCCCCAGAA 250



CTGTGCTGCC TGTGTCTATG AAGGCCTGTA TGAAGAAGGC ATTTCTATTT 300 TAGAGAGTAG TTCGGCCTTT CCAGATAACG CTGCCCGCAG AGAGGTGGAG 350 AGCCTGCCAG CTGTCTGTCC CAATGATGGA TGCACTTGGA AGGGGACCTT 400 GAAAGAATAC GAGAGCTGCC ACGAAGGACT TTGCCCATTC CTGCTGACGG 450 AGTGTCCTGC ATGTAAAGGC CTGGTCCGCC TCAGCGAGAA GGAGCACCAC 500 ACTGAGCAGG AATGCCCCAA AAGGAGCCTG AGCTGCCAGC ACTGCAGAGC 550 ACCCTGTAGC CACGTGGACC TGGAGGTACA CTATGAGGTC TGCCCCAAGT 600 TTCCCTTAAC CTGTGATGGC TGTGGCAAGA AGAAGATCCC TCGGGAGACG 650 TTTCAGGACC ATGTTAGAGC ATGCAGCAAA TGCCGGGTTC TCTGCAGATT 700 CCACACCGTT GGCTGTTCAG AGATGGTGGA GACTGAGAAC CTGCAGGATC 750 ATGAGCTGCA GCGGCTACGG GAACACCTAG CCCTACTGCT GAGCTCATTC 800 TTGGAGGCCC AAGCCTCTCC AGGAACCTTG AACCAGGTGG GGCCAGAGCT 850 ACTCCAGCGG TGCCAGATTT TGGAGCAGAA GATAGCAACC TTTGAGAACA 900 TTGTCTGCGT CTTGAACCGT GAAGTAGAGA GGGTAGCAGT GACTGCAGAG 950 GCTTGTAGCC GGCAGCACCG GCTAGACCAG GACAAGATTG AGGCCCTGAG 1000 TAACAAGGTG CAACAGCTGG AGAGGAGCAT CGGCCTCAAG GACCTGGCCA 1050 TGGCTGACCT GGAGCAGAAG GTCTCCGAGT TGGAAGTATC CACCTATGAT 1100 GGGGTCTTCA TCTGGAAGAT CTCTGACTTC ACCAGAAAGC GTCAGGAAGC 1150 CGTAGCTGGC CGGACACCAG CTATCTTCTC CCCAGCCTTC TACACAAGCA 1200 GATATGGCTA CAAGATGTGT CTACGAGTCT ACTTGAATGG CGACGGCACT 1250 GGGCGGGAA CTCATCTGTC TCTCTTCTTC GTGGTGATGA AAGGCCCCAA 1300

TGATGCTCTG TTGCAGTGGC CTTTTAATCA GAAGGTAACA TTGATGTTGC 1350 TGGACCATAA CAACCGGGAG CATGTGATCG ACGCATTCAG GCCCGATGTA 1400 ACCTCGTCCT CCTTCCAGAG GCCTGTCAGT GACATGAACA TCGCCAGTGG 1450 CTGCCCCTC TTCTGCCCTG TGTCCAAGAT GGAGGCCAAG AATTCCTATG 1500 TGCGGGATGA TGCGATCTTC ATCAAAGCTA TTGTGGACCT AACAGGACTC 1550 TAGCCACCCC TGCTAAGAAT AGCAGCTCAG TGAGGAGCTG TCACATTAGG 1600 CCAGCCAGGC CCTGCCACAC ACGGGTGGGC AGGCTTGGTG TAAATGCTGG 1650 GGAGGCCTC AGCCTAGAGC CAATCACCAT CACACAGAAA GGCAGGAAGA 1700 AGCCTCCAGT TGGCCTTCAG CTGGCAAACT GAGTTGGACG GTCCACTGAG 1750 CTCAAGGGCC TGGTGGAGCC CGCTGGGGAG CTTCTCAGCT TTCCAATAGG 1800 AAAGCTCCTG CTGTCTCCTC TGTCTGGGGA AGGGAGAGAC CTGTAGGTGG 1850 GTGCTCAGAA AGGGCCTCTC CAGAGAGAGT CTCAAGAGCT GCAGCAGGAG 1900 CAAAGTGACT GGCCTTCCCC ACCCCATCCT TTGGAAAAGA GGTAGCGGCT 1950 ACACAGGAGA AGGCATGCGC CTGCAGGGTG TAGCCCAAGA GAGAAGCTCT 2000 CTGAGACATA GGCCCTCACT GGAGAAGGGC CTGCCTGGGC TGCACAGCCT 2050 TGCCAGGTGG CCTGTATGGG GGAGAAGTGA TTAAATGTTG AGATGTCACA 2100 CGACAAAAA AAAAAAAAA A 2121

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

- Met Ala Ala Ser Val Thr Ser Pro Gly Ser Leu Glu Leu Leu 1 5 10 15
- Gln Pro Gly Phe Ser Lys Thr Leu Leu Gly Thr Arg Leu Glu Ala 20 25 30
- Lys Tyr Leu Cys Ser Ala Cys Lys Asn Ile Leu Arg Arg Pro Phe 35 40 45
- Gln Ala Gln Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Thr Ser 50 55 60
- Ile Leu Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val Tyr Glu 65 70 75
- Gly Leu Tyr Glu Glu Gly Ile Ser Ile Leu Glu Ser Ser Ser Ala 80 85 90
- Phe Pro Asp Asn Ala Ala Arg Arg Glu Val Glu Ser Leu Pro Ala 95 100 105
- Val Cys Pro Asn Asp Gly Cys Thr Trp Lys Gly Thr Leu Lys Glu
 110 115 120
- Tyr Glu Ser Cys His Glu Gly Leu Cys Pro Phe Leu Leu Thr Glu 125 130 135
- Cys Pro Ala Cys Lys Gly Leu Val Arg Leu Ser Glu Lys Glu His 140 145 150
- His Thr Glu Gln Glu Cys Pro Lys Arg Ser Leu Ser Cys Gln His 155 160 165
- Cys Arg Ala Pro Cys Ser His Val Asp Leu Glu Val His Tyr Glu 170 175 180
- Val Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys Gly Lys Lys 185 190 195

| Lys Ile Pro Arg Glu | Thr Phe Glr | ı Asp His Val A | Arg Ala Cys Ser |
|---------------------|-------------|-----------------|-----------------|
| 200 | 205 | 210 | |

- Lys Cys Arg Val Leu Cys Arg Phe His Thr Val Gly Cys Ser Glu 215 220 225
- Met Val Glu Thr Glu Asn Leu Gln Asp His Glu Leu Gln Arg Leu 230 235 240
- Arg Glu His Leu Ala Leu Leu Ser Ser Phe Leu Glu Ala Gln 245 250 255
- Ala Ser Pro Gly Thr Leu Asn Gln Val Gly Pro Glu Leu Leu Gln 260 265 270
- Arg Cys Gln Ile Leu Glu Gln Lys Ile Ala Thr Phe Glu Asn Ile 275 280 285
- Val Cys Val Leu Asn Arg Glu Val Glu Arg Val Ala Val Thr Ala 290 295 300
- Glu Ala Cys Ser Arg Gln His Arg Leu Asp Gln Asp Lys Ile Glu 305 310 315
- Ala Leu Ser Asn Lys Val Gln Gln Leu Glu Arg Ser Ile Gly Leu 320 325 330
- Lys Asp Leu Ala Met Ala Asp Leu Glu Gln Lys Val Ser Glu Leu 335 340 345
- Glu Val Ser Thr Tyr Asp Gly Val Phe Ile Trp Lys Ile Ser Asp 350 355 360
- Phe Thr Arg Lys Arg Gln Glu Ala Val Ala Gly Arg Thr Pro Ala 365 370 375
- Ile Phe Ser Pro Ala Phe Tyr Thr Ser Arg Tyr Gly Tyr Lys Met 380 385 390
- Cys Leu Arg Val Tyr Leu Asn Gly Asp Gly Thr Gly Arg Gly Thr 395 400 405

His Leu Ser Leu Phe Phe Val Val Met Lys Gly Pro Asn Asp Ala 410 415 420 Leu Leu Gln Trp Pro Phe Asn Gln Lys Val Thr Leu Met Leu Leu 430 435 Asp His Asn Asn Arg Glu His Val Ile Asp Ala Phe Arg Pro Asp 445 450 Val Thr Ser Ser Ser Phe Gln Arg Pro Val Ser Asp Met Asn Ile 455 460 465 Ala Ser Gly Cys Pro Leu Phe Cys Pro Val Ser Lys Met Glu Ala 470 475 480 Lys Asn Ser Tyr Val Arg Asp Asp Ala Ile Phe Ile Lys Ala Ile 485 490 495 Val Asp Leu Thr Gly Leu 500 501 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: Asp Leu Cys Pro Ile Cys Met Gln Ile Ile Lys Asp Ala Phe 1 5 10 15 Leu Thr Ala Cys Gly His Ser Phe Cys Tyr Met Cys Ile Ile Thr 20 25 30 His Leu Arg Asn Lys Ser Asp Cys Pro Cys Cys Ser Gln His 35 40 44

(2) INFORMATION FOR SEQ ID NO:6:

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| (B) 7 | (A) LENGTH: 47 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear | | | | | |
|---|--|---------------------|-----------------------------------|--|--|--|
| (xi) SEC | QUENCE DES | SCRIPTION | : SEQ ID NO:6: | | | |
| Glu Leu 1 | Ser Cys Ser II | le Cys Leu G 10 | du Pro Phe Lys Glu Pro Val 15 | | | |
| Thr Thr | Pro Cys Gly I 20 | His Asn Phe (25 | Cys Gly Ser Cys Leu Asn Glu 30 | | | |
| Thr Trp | Ala Val Gln C 35 | Gly Ser Pro T 40 | yr Leu Cys Pro Gln Cys Arg 45 | | | |
| Ala Val 47 | | | | | | |
| (2) INFO | RMATION F | OR SEQ ID | NO:7: | | | |
| (A) I (B) 7 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 44 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear | | | | | |
| (xi) SEC | QUENCE DES | SCRIPTION: | : SEQ ID NO:7: | | | |
| Leu Leu 1 | Arg Cys His 1 | lle Cys Lys A 10 | Asp Phe Leu Lys Val Pro Val 15 | | | |
| Leu Thr | Pro Cys Gly I 20 | His Thr Phe C 25 | Cys Ser Leu Cys Ile Arg Thr 30 | | | |
| His Leu Asn Asn Gln Pro Asn Cys Pro Leu Cys Leu Phe Glu 35 40 44 | | | | | | |
| (2) INFO | RMATION F | OR SEQ ID | NO:8: | | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 amino acids | | | | | |

(i) SEQUENCE CHARACTERISTICS:



| • • | YPE: Amino COPOLOGY: I | | |
|----------------|--|---------------------|----------------------------------|
| (xi) SEQ | UENCE DES | SCRIPTION: | SEQ ID NO:8: |
| Ala Phe | Arg Cys His V 5 | /al Cys Lys A 10 | sp Phe Tyr Asp Ser Pro Met 15 |
| Leu Thr | Ser Cys Asn F 20 | His Thr Phe C | ys Ser Leu Cys Ile Arg Arg 30 |
| Cys Leu | Ser Val Asp S 35 | • • | ro Leu Cys Arg Ala Thr 14 |
| (2) INFO | RMATION FO | OR SEQ ID N | IO:9: |
| (A) L (B) T | UENCE CHA ENGTH: 45 a YPE: Amino OPOLOGY: 1 | amino acids Acid | TCS: |
| (xi) SEQ | UENCE DES | CRIPTION: | SEQ ID NO:9: |
| Ser Ile Se | er Cys Gln Ile 5 | Cys Glu His | Ile Leu Ala Asp Pro Val 15 |
| Glu Thr A | Asn Cys Lys I 20 | His Val Phe C 25 | ys Arg Val Cys Ile Leu Arg 30 |
| Cys Leu | Lys Val Met (35 | Gly Ser Tyr C 40 | ys Pro Ser Cys Arg Tyr Pro 45 |
| (2) INFOI | RMATION FO | OR SEQ ID N | IO:10: |
| (A) L (B) T | UENCE CHA ENGTH: 45 a YPE: Amino OPOLOGY: 1 | amino acids Acid | ICS: |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

121

| Glu Val 1 | Thr Cys Pro II 5 | e Cys Leu As 10 | p Pro Phe Val Glu Pro Val 15 |
|----------------|--|----------------------|----------------------------------|
| Ser Ile G | lu Cys Gly Hi 20 | s Ser Phe Cys 25 | Gln Glu Cys Ile Ser Gln 30 |
| Val Gly I | Lys Gly Gly C 35 | Gly Ser Val Cy 40 | vs Ala Val Cys Arg Gln Arg 45 |
| (2) INFOI | RMATION FO | OR SEQ ID N | O:11: |
| (A) L (B) T | UENCE CHA ENGTH: 46 a YPE: Amino OPOLOGY: I | Acid | ICS: |
| (xi) SEQ | UENCE DES | SCRIPTION: S | SEQ ID NO:11: |
| Glu Leu l 1 | Met Cys Pro I 5 | le Cys Leu As 10 | sp Met Leu Lys Asn Thr Met 15 |
| Thr Thr L | Lys Glu Cys L 20 | eu His Arg Pl 25 | ne Cys Ser Asp Cys Ile Val 30 |
| Thr Ala I | Leu Arg Ser G 35 | dly Asn Lys G | lu Cys Pro Thr Cys Arg Lys 45 |
| Lys 46 | | | |
| (2) INFOI | RMATION FO | OR SEQ ID N | O:12: |
| (A) L (B) T | UENCE CHA ENGTH: 50 a YPE: Amino OPOLOGY: 1 | Acid | ICS: |
| (xi) SEQ | UENCE DES | CRIPTION: S | SEQ ID NO:12: |
| Glu Val 7 | Thr Cys Pro Il 5 | e Cys Leu Glu 10 | ı Leu Leu Lys Glu Pro Val 15 |

 $\left(\right)^{2}$

| | 20 | 25 | 30 | |
|----------------|--|----------------------|----------------------------------|---------------|
| Asn Tyr | Glu Ser Asn A 35 | Arg Asn Thr A 40 | Asp Gly Lys Gly Asn Cys Pr 45 | : O |
| Val Cys | Arg Val Pro 50 | | | |
| (2) INFO | RMATION FO | OR SEQ ID N | IO:13: | |
| (A) L (B) T | UENCE CHA ENGTH: 47 a YPE: Amino OPOLOGY: 1 | imino acids Acid | TICS: | |
| (xi) SEQ | UENCE DES | CRIPTION: S | SEQ ID NO:13: | |
| Glu Thr | Γhr Cys Pro V 5 | al Cys Leu G | ln Tyr Phe Ala Glu Pro Met 15 | C |
| Met Leu | Asp Cys Gly 1 20 | His Asn Ile Cy 25 | ys Cys Ala Cys Leu Ala Arg 30 | g |
| Cys Trp | Gly Thr Ala G 35 | du Thr Asn Va 40 | al Ser Cys Pro Gln Cys Arg 45 | r , |
| Glu Thr 47 | | | | |
| (2) INFO | RMATION FO | OR SEQ ID N | O:14: | |
| (A) L (B) T | UENCE CHA ENGTH: 48 a YPE: Amino A OPOLOGY: I | mino acids Acid | TCS: | |
| (xi) SEQ | UENCE DES | CRIPTION: S | SEQ ID NO:14: | |
| Phe Gln l | Leu Cys Lys I 5 | le Cys Ala Gl | u Asn Asp Lys Asp Val Lys 15 | S |
| | | | 123 | |

Ser Ala Asp Cys Asn His Ser Phe Cys Arg Ala Cys Ile Thr Leu

| Ile Glu Pro | o Cys Gly His 20 | s Leu Met Cy 25 | ys Thr Ser Cys Leu Thr Ser 30 |
|------------------|--|-----------------------|-----------------------------------|
| Trp Gln G | du Ser Glu Gl 35 | y Gln Gly So 40 | er Ser Gly Cys Pro Phe Cys 45 |
| Arg Cys C | ilu | | |
| (2) INFOR | MATION FO | R SEQ ID N | NO:15: |
| (A) LE (B) TY | JENCE CHAI ENGTH: 28 au (PE: Amino A DPOLOGY: L | mino acids Acid | TICS: |
| (xi) SEQU | JENCE DES | CRIPTION: | SEQ ID NO:15: |
| Gly Gly P | he Lys Leu V 5 | al Thr Cys A | Asp Phe Cys Lys Arg Asp Asp 15 |
| Ile Lys Ly | rs Lys Glu Lei 20 | u Glu Thr Hi 25 28 | s Tyr Lys Thr Cys |
| (2) INFOR | MATION FO | R SEQ ID N | NO:16: |
| (A) LE (B) TY | JENCE CHAI ENGTH: 26 aı (PE: Amino A DPOLOGY: L | mino acids Acid | TICS: |
| (xi) SEQU | JENCE DESC | CRIPTION: | SEQ ID NO:16: |
| Gln Asp L | eu Ala Val C | ys Asp Val (10 | Cys Asn Arg Lys Phe Arg His 15 |
| Lys Asp T | yr Leu Arg A 20 | sp His Gln I 25 26 | Lys Thr His |
| (2) INFOR | MATION FO | R SEQ ID N | IO:17: |



| (A) I (B) T | UENCE CHA LENGTH: 28 a YPE: Amino OPOLOGY: | amino acids Acid | TICS: |
|----------------|--|-------------------------|-----------------------------------|
| (xi) SEC | QUENCE DES | SCRIPTION: | SEQ ID NO:17: |
| Thr Gly 1 | Lys Tyr Pro Pi 5 | he Ile Cys Se 10 | er Glu Cys Gly Lys Ser Phe 15 |
| Met Asp | Lys Arg Tyr l 20 | Leu Lys Ile H 25 28 | Iis Ser Asn Val His |
| (2) INFO | RMATION FO | OR SEQ ID 1 | NO:18: |
| (A) L (B) T | UENCE CHA ENGTH: 28 a YPE: Amino OPOLOGY: 1 | amino acids Acid | TICS: |
| (xi) SEC | UENCE DES | CRIPTION: | SEQ ID NO:18: |
| Thr Gly | Glu Lys Pro T 5 | yr Thr Cys T 10 | Thr Val Cys Gly Lys Lys Phe 15 |
| Ile Asp A | Arg Ser Ser Va 20 | al Val Lys His 25 28 | s Ser Arg Thr His |
| (2) INFO | RMATION FO | OR SEQ ID N | NO:19: |
| (A) L (B) T | UENCE CHA ENGTH: 28 a YPE: Amino OPOLOGY: 1 | nmino acids Acid | ΓICS: |
| (xi) SEQ | UENCE DES | CRIPTION: | SEQ ID NO:19: |
| Arg Lys | Lys Phe Pro H 5 | lis Ile Cys Gl 10 | ly Glu Cys Gly Lys Gly Phe 15 |



| Arg His | Pro Ser Ala L 20 | eu Lys Ly 25 | ys His 28 | s lie Arg Val His | |
|----------------|--|-------------------|--------------|-----------------------------|--------|
| (2) INFO | RMATION F | OR SEQ | ID N | O:20: | |
| (A) I (B) T | UENCE CHA LENGTH: 28 YPE: Amino OPOLOGY: | amino ac Acid | | CS: | |
| (xi) SEC | QUENCE DES | SCRIPTI | ON: S | EQ ID NO:20: | |
| Ser Glu (| Glu Lys Pro P 5 | he Glu C 10 | ys Gl | u Glu Cys Gly Lys I 15 | ys Phe |
| Arg Thr | Ala Arg His I 20 | Leu Val L 25 | ys Hi 28 | s Gln Arg Ile His | |
| (2) INFO | RMATION F | OR SEQ | ID N | O:21: | |
| (A) L (B) T | UENCE CHA ENGTH: 28 YPE: Amino OPOLOGY: | amino aci Acid | | CS: | |
| (xi) SEQ | QUENCE DES | SCRIPTIO | ON: S | EQ ID NO:21: | |
| Pro Asn | Glu Gln Met . 5 | Ala Gln (10 | Cys Pr | ro Ile Cys Gln Gln Pl 15 | he Tyr |
| Pro Leu l | Lys Ala Leu (20 | Glu Lys T 25 | | s Leu Asp Glu Cys | |
| (2) INFO | RMATION F | OR SEQ | ID N | O:22: | |
| (A) L (B) T | UENCE CHA ENGTH: 28 : YPE: Amino OPOLOGY: | amino aci Acid | | .CS: | |
| (xi) SEQ | UENCE DES | SCRIPTIO | ON: S | EQ ID NO:22: | |

| Pro Asp | Asp Gly L | eu Val Ala (| Cys Pro | Ile Cys | Leu Thr Arg | Met |
|----------|-------------------|--------------------|---------------|---------|-------------|-----|
| 1 | 5 | 10 | 1 | 15 | | |
| Lys Gh | ı Gln Gln V 20 | al Asp Arg I 25 | His Leu 28 | Asp Th | r Ser Cys | |
| (2) INFO | ORMATIO | N FOR SEQ | ID NO | :23: | | |
| (i) SE(| OUENCE C | CHARACTE | RISTIC | S: | | |
| ` ' | • | 21 base pairs | | | | |
| (B) | TYPE: Nuc | leic Acid | | | | |
| (C) | STRANDE | DNESS: Sin | gle | | | |
| (D) | TOPOLOG | Y: Linear | | | | |
| (xi) SE | QUENCE I | DESCRIPTIO | ON: SE | Q ID NO | D:23: | |
| CCTTC | TGCCT G | CAGAGAG | AA G 2 | :1 | | |
| (2) INFO | ORMATIO | N FOR SEQ | ID NO | :24: | | |
| (i) SE | OUENCE C | HARACTE | RISTIC | S: | | |
| ` ' | ~ | 35 base pairs | | | | |
| , , | TYPE: Nuc | - | | | | |
| (C) | STRANDE | DNESS: Sin | gle | | | |
| (D) | TOPOLOG | Y: Linear | | | | |
| (xi) SE | QUENCE I | DESCRIPTIO | ON: SE | Q ID NO | D:24: | |
| CTAGO | GTTAAC T | TTCGGTGC | ст ссс | CAGCA | AGG GTCTC | 35 |

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:25:

(A) LENGTH: 35 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

(28

CTAGGTTAAC TGGAGAAGGG GACCTGCTCG TCCTT 35

- (2) INFORMATION FOR SEQ ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTAGGTTAAC TGCTGGCTTG GGAGGAGCAC TGTGA 35

- (2) INFORMATION FOR SEQ ID NO:27:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
- CTAGGTTAAC TGCTCCCGGT GCTGGCCCGG GCCTC 35
- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGGTTAAC TGCACTGGCC GAGCTCTCCA GGGA 34

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- (2) INFORMATION FOR SEQ ID NO:29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
- **GTGATGAGAA TTCAT 15**
- (2) INFORMATION FOR SEQ ID NO:30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
- **CGATGAATTC TCATCACTGC A 21**
- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
- GATCGGATCC AAAAAGAAGC CCTTGTGCCT GCA 33
- (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs(B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCTGGTTAA CTGGGC 16

- (2) INFORMATION FOR SEQ ID NO:33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCNCCNATGG CNYTNGARC 19

- (2) INFORMATION FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCNCCNATGG CNYTNGARA 19

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCNCCNATGG CNYTNGARG 19

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GYTCNARNGC CATNGGNGC 19

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TYTCNARNGC CATNGGNGC 19

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single

- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CYTCNARNGC CATNGGNGC 19

- (2) INFORMATION FOR SEQ ID NO:39:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AARCAYGCNT AYGTNAA 17

- (2) INFORMATION FOR SEQ ID NO:40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTNACRTANG CRTGYTT 17

- (2) INFORMATION FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

| Ala Pro Met Ala Leu Glu Arg 1 5 7 |
|---|
| (2) INFORMATION FOR SEQ ID NO:42: |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 6 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42: |
| Lys His Ala Tyr Val Lys 1 5 6 |
| (2) INFORMATION FOR SEQ ID NO:43: |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 7 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43: |
| Pro Gly Ser Asn Leu Gly Ser 1 5 7 |
| (2) INFORMATION FOR SEQ ID NO:44: |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 8 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44: |
| Lys Asp Asp Thr Met Phe Leu Lys 1 5 8 |
| (2) INFORMATION FOR SEQ ID NO:45: |



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs(B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCGATCGTCG ACCAAAAAGA AGCCCTCCTG CCTACAA 37

- (2) INFORMATION FOR SEQ ID NO:46:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTAGAGATCT CAGGGGTCAG GCCACTTT 28

- (2) INFORMATION FOR SEQ ID NO:47:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTAGAGATCT GTTAACTTTC GGTGCTCCCC AGCAGGGTCT C 41

- (2) INFORMATION FOR SEQ ID NO:48:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs



(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTAGAGATCT GTTAACTGGA GAAGGGGACC TGCTCGTCCT T 41

- (2) INFORMATION FOR SEQ ID NO:49:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTAGAGATCT GTTAACTGCT GGCTTGGGAG GAGCACTGTG A 41

- (2) INFORMATION FOR SEQ ID NO:50:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCGATCGTCG ACCGCCTCCA GCTCAGCCCC TGAT 34

- (2) INFORMATION FOR SEQ ID NO:51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single



- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATCGGATCC GGAGACACAG ATTCCAGCCC C 31

- (2) INFORMATION FOR SEQ ID NO:52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCGAATTC TTAACTCTTC GGTGCTCCCC AGCAG 35

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCTGGCTGGC CTAATGT 17

- (2) INFORMATION FOR SEQ ID NO:55:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATCGACTCG AGATGCCCAA GAAGAAGCGG AAGGTGGCTG CAGCCAGTGT 50

GACTTCCCCT 60

- (2) INFORMATION FOR SEQ ID NO:56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTCTGGCGAA GAAGTCC 17

- (2) INFORMATION FOR SEQ ID NO:57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GATCGGATCC GCCTCCAGCT CAGCCCCTGA T 31

- (2) INFORMATION FOR SEQ ID NO:58:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GATCGGATCC AGCCAGCAGC TTCTCCTTCA C 31

- (2) INFORMATION FOR SEQ ID NO:59:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GATCGGATCC GCTCAGGCTC TTTTGGGGCA 30

SEQUENCE LISTING

| (1) G | SENERAL | INFORM | MATION: |
|-------|---------|--------|---------|
|-------|---------|--------|---------|

5 (i) APPLICANT: Goeddel, David V. Rothe, Mike

(ii) TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors

10 (iii) NUMBER OF SEQUENCES: 62

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.

(B) STREET: 460 Point San Bruno Blvd

(C) CITY: South San Francisco

(D) STATE: California (E) COUNTRY: USA (F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: patin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 27-May-1994

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

35 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Ginger R.

(B) REGISTRATION NUMBER: 33,055

(C) REFERENCE/DOCKET NUMBER: 897

40 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-3216

(B) TELEFAX: 415/952-9881

(C) TELEX: 910/371-7168

45 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2088 bases

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCAGCCGG TTCTCTGCCC CAAGGACGCT ACCGCCCAAT GCGAGCAGAA 50 GGCGGCGCAC AGATACAGAA AGTGAGGCTC AGACATATTG AAGACCGTGT 100 GACATAGGGT AGCCAAATGA CAGTGTGAGA AAGTGACATT TACTCAAGGC 150 CACCCAGATA TCCTGGAGGA CCCAGAACCC TGGAGATTCC CATCAGAAAG 200 ACCTTCTGGC CACCTGAAAC CCCAAGATGG CCTCCAGCTC AGCCCCTGAT 250 GAAAACGAGT TTCAATTTGG TTGCCCCCCT GCTCCCTGCC AGGACCCATC 300 GGAGCCCAGA GTTCTCTGCT GCACAGCCTG TCTCTCTGAG AACCTGAGAG 350 ATGATGAGGA TCGGATCTGT CCTAAATGCA GAGCAGACAA CCTCCATCCT 400 GTGAGCCCAG GAAGCCCTCT GACTCAGGAG AAGGTTCACT CTGATGTAGC 450 TGAGGCTGAA ATCATGTGCC CCTTTGCAGG TGTTGGCTGT TCCTTCAAGG 500 GGAGCCCACA ATCCATGCAG GAGCATGAGG CTACCTCCCA GTCCTCCCAC 550 CTGTACCTGC TGCTGGCGGT CTTAAAGGAG TGGAAATCCT CACCAGGCTC 600 CAACCTAGGG TCTGCACCCA TGGCACTGGA GCGGAACCTG TCAGAGCTGC 650 AGCTTCAGGC AGCTGTGGAA GCGACAGGGG ACCTGGAGGT AGACTGCTAC 700

CGGGCACCTT GCTGTGAGAG CCAGGAAGAA CTGGCCCTGC AGCACTTGGT 750 GAAGGAGAAG CTGCTGGCTC AGCTGGAGGA GAAGCTGCGT GTGTTTGCAA 800 ACATTGTTGC TGTCCTCAAC AAGGAAGTGG AGGCTTCCCA CCTGGCACTG 850 GCCGCCTCCA TCCACCAGAG CCAGTTGGAC CGAGAGCACC TCCTGAGCTT 900 GGAGCAGAGG GTGGTGGAAT TACAGCAAAC CCTGGCTCAA AAAGACCAGG 950 TCCTGGGCAA GCTTGAGCAC AGTCTGCGAC TCATGGAGGA GGCATCCTTT 1000 GATGGTACTT TCCTGTGGAA GATCACCAAT GTCACCAAGC GGTGCCACGA 1050 GTCAGTGTGT GGCCGGACTG TCAGCCTCTT CTCTCCAGCT TTCTACACTG 1100 CCAAGTATGG TTACAAGTTG TGCCTGCGCT TGTACCTGAA CGGGGATGGC 1150 TCAGGCAAGA AGACCCACCT GTCCCTCTTC ATCGTGATCA TGAGAGGAGA 1200 ATACGATGCT CTCCTGCCCT GGCCTTTCAG GAACAAGGTC ACCTTTATGC 1250 TACTTGACCA GAACAACCGA GAGCATGCTA TTGATGCCTT CCGGCCTGAC 1300 CTGAGCTCAG CCTCCTTCCA GCGGCCACAG AGTGAGACCA ACGTGGCCAG 1350 CGGCTGCCCG CTCTTCTTCC CCCTCAGCAA GCTGCAGTCA CCCAAGCACG 1400 CCTACGTCAA AGATGACACA ATGTTCCTCA AATGCATTGT GGACACTAGT 1450 GCTTAGGGAT GGGGGGAGGG GGTGTCTCCT GACAGAACCA GCTTAGACTG 1500

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| | GGGGACTTAG CTAGACAGCC AGGCCCTGCC TGCCCTTGGA GCCCACAGCC 1990 |
|----|---|
| 5 | CACGACAAGG AGGAGCCAAG GCTGGCATGA CTTCAGCGCC ACAGCATGCT 1600 |
| | GGTTATGGCT GATGTGAGGC TGGAGAAACG TGTGCGTACA GAGACAGAGT 1650 |
| 10 | GGAGGAGAAG ACAGAAGTGC TCTTTTCACA CAGACTACAC GACACCAGGA 1700 |
| | GGCCAGCATG CCAGCAGCTT CTGAATGTTG AGACCAGCCT AGATCAGGAT 1750 |
| 15 | GAAAAGAGCC AGGCCTGAGG CTTGGACATT GAGCCAAGGC TATGGGGCCT 1800 |
| 20 | AAGTGGAGGG GCACTCCTAC CAGGACATTC TCTCGAGGTC AGGGCATAAC 1850 |
| | TGGAAAAATG CCCCCATCTC TCTGTTCAGA CTCAAAACTA GAACCACAGG 1900 |
| 25 | GCAGAAGGGT CAGACATTAA TGTGAATTTA ACCTGCCCTG GACTGAGTTC 1950 |
| | CTATGTTAAC AGACACGCAA ACAGGTAAAC CCAGAAACTG CCCTGGGAAA 2000 |
| 30 | TGCTTTCTGG CTGCATCTGG AGATCTTTGA TGTTTTTACC GACAAAACAA 2050 |
| 35 | ATAACAAAAG CCTTGAATTG CAAAAAAAAA AAAAAAAA 2088 |
| | |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Ser Ser Ala Pro Asp Glu Asn Glu Phe Gln Phe Gly 1 5 10 15

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| | Cys Pro Pro Ala Pro Cys Gln Asp Pro Ser Glu Pro Arg Val Leu 20 25 30 |
|----|--|
| 5 | Cys Cys Thr Ala Cys Leu Ser Glu Asn Leu Arg Asp Asp Glu Asp 35 40 45 |
| | Arg lle Cys Pro Lys Cys Arg Ala Asp Asn Leu His Pro Val Ser 50 55 60 |
| 10 | Pro Gly Ser Pro Leu Thr Gln Glu Lys Val His Ser Asp Val Ala 65 70 75 |
| 15 | Glu Ala Glu Ile Met Cys Pro Phe Ala Gly Val Gly Cys Ser Phe 80 85 90 |
| 15 | Lys Gly Ser Pro Gln Ser Met Gln Glu His Glu Ala Thr Ser Gln 95 100 105 |
| 20 | Ser Ser His Leu Tyr Leu Leu Leu Ala Val Leu Lys Glu Trp Lys 110 115 120 |
| | Ser Ser Pro Gly Ser Asn Leu Gly Ser Ala Pro Met Ala Leu Glu 125 130 135 |
| 25 | Arg Asn Leu Ser Glu Leu Gln Leu Gln Ala Ala Val Glu Ala Thr 140 145 150 |
| 20 | Gly Asp Leu Glu Val Asp Cys Tyr Arg Ala Pro Cys Cys Glu Ser 155 160 165 |
| 30 | Gln Glu Glu Leu Ala Leu Gln His Leu Val Lys Glu Lys Leu Leu 170 175 180 |
| 35 | Ala Gin Leu Giu Giu Lys Leu Arg Vai Phe Ala Asn ile Vai Ala 185 190 195 |
| | Val Leu Asn Lys Glu Val Glu Ala Ser His Leu Ala Leu Ala Ala 200 205 210 |
| 40 | Ser Ile His Gln Ser Gln Leu Asp Arg Glu His Leu Leu Ser Leu 215 220 225 |
| 45 | Glu Gln Arg Val Val Glu Leu Gln Gln Thr Leu Ala Gln Lys Asp 230 235 240 |
| 45 | Gln Val Leu Gly Lys Leu Glu His Ser Leu Arg Leu Met Glu Glu 245 250 255 |

| | Ala Ser Phe Asp Gly Thr Phe Leu 260 265 | Trp Lys lie Thr Asn Val Thr 270 | |
|----|---|------------------------------------|--------------|
| 5 | Lys Arg Cys His Glu Ser Val Cys 275 280 | Gly Arg Thr Val Ser Leu Phe 285 | |
| | Ser Pro Ala Phe Tyr Thr Ala Lys 1 290 295 | Tyr Gly Tyr Lys Leu Cys Leu 300 | |
| 10 | Arg Leu Tyr Leu Asn Gly Asp Gly 305 310 | Ser Gly Lys Lys Thr His Leu 315 | |
| 15 | Ser Leu Phe Ile Val Ile Met Arg G 320 325 | ly Glu Tyr Asp Ala Leu Leu 330 | |
| | Pro Trp Pro Phe Arg Asn Lys Val 335 340 | Thr Phe Met Leu Leu Asp Gin 345 | |
| 20 | Asn Asn Arg Glu His Ala Ile Asp 350 355 | Ala Phe Arg Pro Asp Leu Ser 360 | |
| | Ser Ala Ser Phe Gln Arg Pro Gln 3 365 370 | Ser Glu Thr Asn Val Ala Ser 375 | |
| 25 | Gly Cys Pro Leu Phe Phe Pro Leu 380 385 | Ser Lys Leu Gln Ser Pro Lys 390 | |
| 30 | His Ala Tyr Val Lys Asp Asp Thr 395 400 | Met Phe Leu Lys Cys Ile Val 405 | |
| | Asp Thr Ser Ala 409 | | |
| 35 | (2) INFORMATION FOR SEQ ID NO | 0:3: | |
| | (i) SEQUENCE CHARACTERISTI (A) LENGTH: 2121 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single | CS: | |
| 10 | (D) TOPOLOGY: linear | | |
| | (xi) SEQUENCE DESCRIPTION: S | SEQ ID NO:3: | |
| 15 | GCGCGAAGAC CGTTGGGGCT T | TTGTGGTGTG TGGGGGTTGT AA | CTCACATG 50 |
| | GCTGCAGCCA GTGTGACTTC C | CCTGGCTCC CTAGAACTGC TAG | CAGCCTGG 100 |

CTTCTCCAAG ACCCTCCTGG GGACCAGGTT AGAAGCCAAG TACCTCTGTT 150 CAGCCTGCAA AAACATCCTG CGGAGGCCTT TCCAGGCCCA GTGTGGGCAC 200 CGCTACTGCT CCTTCTGCCT GACCAGCATC CTCAGCTCTG GGCCCCAGAA 250 CTGTGCTGCC TGTGTCTATG AAGGCCTGTA TGAAGAAGGC ATTTCTATTT 300 TAGAGAGTAG TTCGGCCTTT CCAGATAACG CTGCCCGCAG AGAGGTGGAG 350 AGCCTGCCAG CTGTCTGTCC CAATGATGGA TGCACTTGGA AGGGGACCTT 400 GAAAGAATAC GAGAGCTGCC ACGAAGGACT TTGCCCATTC CTGCTGACGG 450 AGTGTCCTGC ATGTAAAGGC CTGGTCCGCC TCAGCGAGAA GGAGCACCAC 500 ACTGAGCAGG AATGCCCCAA AAGGAGCCTG AGCTGCCAGC ACTGCAGAGC 550 ACCCTGTAGC CACGTGGACC TGGAGGTACA CTATGAGGTC TGCCCCAAGT 600 TTCCCTTAAC CTGTGATGGC TGTGGCAAGA AGAAGATCCC TCGGGAGACG 650 TTTCAGGACC ATGTTAGAGC ATGCAGCAAA TGCCGGGTTC TCTGCAGATT 700 CCACACCGTT GGCTGTTCAG AGATGGTGGA GACTGAGAAC CTGCAGGATC 750 ATGAGCTGCA GCGGCTACGG GAACACCTAG CCCTACTGCT GAGCTCATTC 800 TTGGAGGCCC AAGCCTCTCC AGGAACCTTG AACCAGGTGG GGCCAGAGCT 850 ACTCCAGCGG TGCCAGATTT TGGAGCAGAA GATAGCAACC TTTGAGAACA 900

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TTGTCTGCGT CTTGAACCGT GAAGTAGAGA GGGTAGCAGT GACTGCAGAG 950 GCTTGTAGCC GGCAGCACCG GCTAGACCAG GACAAGATTG AGGCCCTGAG 1000 TAACAAGGTG CAACAGCTGG AGAGGAGCAT CGGCCTCAAG GACCTGGCCA 1050 TGGCTGACCT GGAGCAGAAG GTCTCCGAGT TGGAAGTATC CACCTATGAT 1100 **GGGGTCTTCA TCTGGAAGAT CTCTGACTTC ACCAGAAAGC GTCAGGAAGC 1150** CGTAGCTGGC CGGACACCAG CTATCTTCTC CCCAGCCTTC TACACAAGCA 1200 GATATGGCTA CAAGATGTGT CTACGAGTCT ACTTGAATGG CGACGGCACT 1250 GGGCGGGAA CTCATCTGTC TCTCTTCTTC GTGGTGATGA AAGGCCCCAA 1300 TGATGCTCTG TTGCAGTGGC CTTTTAATCA GAAGGTAACA TTGATGTTGC 1350 TGGACCATAA CAACCGGGAG CATGTGATCG ACGCATTCAG GCCCGATGTA 1400 ACCTCGTCCT CCTTCCAGAG GCCTGTCAGT GACATGAACA TCGCCAGTGG 1450 CTGCCCCCTC TTCTGCCCTG TGTCCAAGAT GGAGGCCAAG AATTCCTATG 1500 TGCGGGATGA TGCGATCTTC ATCAAAGCTA TTGTGGACCT AACAGGACTC 1550 TAGCCACCC TGCTAAGAAT AGCAGCTCAG TGAGGAGCTG TCACATTAGG 1600 CCAGCCAGGC CCTGCCACAC ACGGGTGGGC AGGCTTGGTG TAAATGCTGG 1650 GGAGGGCCTC AGCCTAGAGC CAATCACCAT CACACAGAAA GGCAGGAAGA 1700

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| | AGCCTCCAGT TGGCCTTCAG CTGGCAAACT GAGTTGGACG GTCCACTGAG 1750 |
|----|---|
| 5 | CTCAAGGGCC TGGTGGAGCC CGCTGGGGAG CTTCTCAGCT TTCCAATAGG 1800 |
| | AAAGCTCCTG CTGTCTCCTC TGTCTGGGGA AGGGAGAGC CTGTAGGTGG 1850 |
| 10 | GTGCTCAGAA AGGGCCTCTC CAGAGAGAT CTCAAGAGCT GCAGCAGGAG 1900 |
| | CAAAGTGACT GGCCTTCCCC ACCCCATCCT TTGGAAAAGA GGTAGCGGCT 1950 |
| 15 | ACACAGGAGA AGGCATGCGC CTGCAGGGTG TAGCCCAAGA GAGAAGCTCT 2000 |
| 20 | CTGAGACATA GGCCCTCACT GGAGAAGGGC CTGCCTGGGC TGCACAGCCT 2050 |
| | TGCCAGGTGG CCTGTATGGG GGAGAAGTGA TTAAATGTTG AGATGTCACA 2100 |
| 25 | CGACAAAAA AAAAAAAAA A 2121 |

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Ala Ser Val Thr Ser Pro Gly Ser Leu Glu Leu Leu

1 5 10 15

40

45

Gin Pro Gly Phe Ser Lys Thr Leu Leu Gly Thr Arg Leu Glu Ala

20 25 30

Lys Tyr Leu Cys Ser Ala Cys Lys Asn lle Leu Arg Arg Pro Phe

35 40 45

Gln Ala Gln Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Thr Ser

50 55 60

| | lle Leu Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val Tyr Glu 65 70 75 |
|----|--|
| 5 | Gly Leu Tyr Glu Glu Gly lle Ser lle Leu Glu Ser Ser Ser Ala 80 85 90 |
| | Phe Pro Asp Asn Ala Ala Arg Arg Glu Val Glu Ser Leu Pro Ala 95 100 105 |
| 10 | Val Cys Pro Asn Asp Gly Cys Thr Trp Lys Gly Thr Leu Lys Glu 110 115 120 |
| 15 | Tyr Glu Ser Cys His Glu Gly Leu Cys Pro Phe Leu Leu Thr Glu 125 130 135 |
| 15 | Cys Pro Ala Cys Lys Gly Leu Val Arg Leu Ser Glu Lys Glu His 140 145 150 |
| 20 | His Thr Glu Gln Glu Cys Pro Lys Arg Ser Leu Ser Cys Gln His 155 160 165 |
| , | Cys Arg Ala Pro Cys Ser His Val Asp Leu Glu Val His Tyr Glu 170 175 180 |
| 25 | Val Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys Gly Lys Lys 185 190 195 |
| 20 | Lys lle Pro Arg Glu Thr Phe Gln Asp His Val Arg Ala Cys Ser 200 205 210 |
| 30 | Lys Cys Arg Val Leu Cys Arg Phe His Thr Val Gly Cys Ser Glu 215 220 225 |
| 35 | Met Val Glu Thr Glu Asn Leu Gln Asp His Glu Leu Gln Arg Leu 230 235 240 |
| | Arg Glu His Leu Ala Leu Leu Ser Ser Phe Leu Glu Ala Gln 245 250 255 |
| 40 | Ala Ser Pro Gly Thr Leu Asn Gln Val Gly Pro Glu Leu Leu Gln 260 265 270 |
| 45 | Arg Cys Gin Ile Leu Giu Gin Lys Ile Ala Thr Phe Giu Asn Ile 275 280 285 |
| 45 | Val Cys Val Leu Asn Arg Glu Val Glu Arg Val Ala Val Thr Ala 290 295 300 |

| | Glu Ala Cy | s Ser Arg Gln Hi 305 | is Arg Leu Asp (310 | Gln Asp Lys Ile Glu 315 |
|-----|------------------|--|--------------------------|----------------------------|
| 5 | Ala Leu Se | er Asn Lys Val G 320 | In Gin Leu Glu A 325 | arg Ser lle Gly Leu 330 |
| | Lys Asp Le | eu Ala Met Ala A 335 | asp Leu Glu Gln 340 | Lys Val Ser Glu Leu 345 |
| 10 | Glu Val Se | r Thr Tyr Asp Gl 350 | y Val Phe lle Trp 355 | Lys lle Ser Asp 360 |
| 15 | Phe Thr Ai | rg Lys Arg Gin G 365 | lu Ala Val Ala G 370 | ly Arg Thr Pro Ala 375 |
| 13 | lle Phe Ser | Pro Ala Phe Tyr 380 | Thr Ser Arg Ty 385 | r Gly Tyr Lys Met 390 |
| 20 | Cys Leu A | rg Val Tyr Leu A 395 | sn Gly Asp Gly 400 | Thr Gly Arg Gly Thi 405 |
| | His Leu Se | r Leu Phe Phe V 410 | al Val Met Lys 0 415 | Gly Pro Asn Asp Ala 420 |
| 25 | Leu Leu Gi | n Trp Pro Phe A 425 | sn Gin Lys Val T 430 | Thr Leu Met Leu Leu 435 |
| 3.0 | Asp His As | sn Asn Arg Glu I 440 | His Val IIe Asp A 445 | ala Phe Arg Pro Asp 450 |
| 30 | Val Thr Se | r Ser Ser Phe Gl | n Arg Pro Val Se 460 | er Asp Met Asn Ile 465 |
| 35 | Ala Ser Gl | y Cys Pro Leu Ph 470 | ne Cys Pro Val S 475 | er Lys Met Glu Ala 480 |
| | Lys Asn S | er Tyr Val Arg A 485 | • | he lle Lys Ala lle 495 |
| 40 | Val Asp Le | eu Thr Gly Leu 500 501 | | |
| | (2) INFORM | MATION FOR SEC | Q ID NO:5: | |
| 45 | (A) LE (B) TY | ENCE CHARACT NGTH: 44 amino PE: amino acid | o acids | |

| 5 | Asp Leu Le 1 | u Cys Pro lle Cy 5 | s Met Gin Ile 10 | lle Lys Asp Ala Phe 15 |
|----|--------------------|---|----------------------|-----------------------------|
| 5 | Leu Thr Ala | Cys Gly His Se 20 | er Phe Cys Tyl 25 | Met Cys lle lle Thr 30 |
| 10 | His Leu Arg | Asn Lys Ser A 35 | sp Cys Pro Cy 40 | vs Cys Ser Gln His 44 |
| | (2) INFORM | ATION FOR SEC | Q ID NO:6: | |
| 15 | (A) LEN (B) TYF | NCE CHARACT IGTH: 47 amino PE: amino acid POLOGY: linear | | |
| 20 | (xi) SEQUE | NCE DESCRIPT | ION: SEQ ID I | NO:6: |
| | Glu Leu Ser 1 | Cys Ser Ile Cys | s Leu Glu Pro 10 | Phe Lys Glu Pro Val 15 |
| 25 | Thr Thr Pro | Cys Gly His As 20 | n Phe Cys Gly 25 | y Ser Cys Leu Asn Glu 30 |
| | Thr Trp Ala | Val Gln Gly Se 35 | r Pro Tyr Leu 40 | Cys Pro Gln Cys Arg 45 |
| 30 | Ala Val 47 | | | |
| | (2) INFORM | ATION FOR SEC | 2 ID NO:7: | |
| 35 | (A) LEN | NCE CHARACT IGTH: 44 amino PE: amino acid POLOGY: linear | | |
| 10 | (xi) SEQUE | NCE DESCRIPT | ION: SEQ ID I | NO:7: |
| | Leu Leu Arg 1 | Cys His Ile Cy 5 | s Lys Asp Phe 10 | e Leu Lys Val Pro Val 15 |
| 15 | Leu Thr Pro | Cys Gly His Th 20 | or Phe Cys Sei 25 | Leu Cys lle Arg Thr 30 |
| | His Leu Asr | n Asn Gln Pro A | sn Cys Pro Le | eu Cys Leu Phe Glu |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

(2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: 5 (A) LENGTH: 44 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: 10 Ala Phe Arg Cys His Val Cys Lys Asp Phe Tyr Asp Ser Pro Met 5 10 1 Leu Thr Ser Cys Asn His Thr Phe Cys Ser Leu Cys Ile Arg Arg 15 25 Cys Leu Ser Val Asp Ser Lys Cys Pro Leu Cys Arg Ala Thr 40 44 20 (2) INFORMATION FOR SEQ ID NO:9: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 amino acids (B) TYPE: amino acid 25 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: Ser Ile Ser Cys Gln Ile Cys Glu His Ile Leu Ala Asp Pro Val 30 5 10 15 1 Glu Thr Asn Cys Lys His Val Phe Cys Arg Val Cys Ile Leu Arg 25 20 35 Cys Leu Lys Val Met Gly Ser Tyr Cys Pro Ser Cys Arg Tyr Pro 35 40 45 (2) INFORMATION FOR SEQ ID NO:10: 40 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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| | Glu Val Thr Cys Pro Ile Cys Leu Asp Pro Phe Val Glu Pro Val 1 5 10 15 |
|----|--|
| 5 | Ser Ile Glu Cys Gly His Ser Phe Cys Gln Glu Cys Ile Ser Gln 20 25 30 |
| | Val Gly Lys Gly Gly Ser Val Cys Ala Val Cys Arg Gln Arg 35 40 45 |
| 10 | (2) INFORMATION FOR SEQ ID NO:11: |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11: |
| 20 | Glu Leu Met Cys Pro Ile Cys Leu Asp Met Leu Lys Asn Thr Met 1 5 10 15 |
| 25 | Thr Thr Lys Glu Cys Leu His Arg Phe Cys Ser Asp Cys Ile Val 20 25 30 |
| 23 | Thr Ala Leu Arg Ser Gly Asn Lys Glu Cys Pro Thr Cys Arg Lys 35 40 45 |
| 30 | Lys 46 |
| | (2) INFORMATION FOR SEQ ID NO:12: |
| 35 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 50 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: |
| | Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Lys Glu Pro Val 1 5 10 15 |
| 45 | Ser Ala Asp Cys Asn His Ser Phe Cys Arg Ala Cys Ile Thr Leu 20 25 30 |
| | Asn Tyr Glu Ser Asn Arg Asn Thr Asp Gly Lys Gly Asn Cys Pro 35 40 45 |
| | |

50 (2) INFORMATION FOR SEQ ID NO:13: 5 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 47 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: Glu Thr Thr Cys Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met 10 15 15 Met Leu Asp Cys Gly His Asn Ile Cys Cys Ala Cys Leu Ala Arg 25 Cys Trp Gly Thr Ala Glu Thr Asn Val Ser Cys Pro Gln Cys Arg 40 20 Glu Thr 47 (2) INFORMATION FOR SEQ ID NO:14: 25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 amino acids (B) TYPE: amino acid 30 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14: Phe Gin Leu Cys Lys Ile Cys Ala Glu Asn Asp Lys Asp Val Lys 10 35 lle Glu Pro Cys Gly His Leu Met Cys Thr Ser Cys Leu Thr Ser 20 25 Trp Gln Glu Ser Glu Gly Gln Gly Ser Ser Gly Cys Pro Phe Cys 40 45 40 35 Arg Cys Glu 48 45

Val Cys Arg Val Pro

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15: 5 Gly Gly Phe Lys Leu Vai Thr Cys Asp Phe Cys Lys Arg Asp Asp 5 10 15 1 lle Lys Lys Glu Leu Glu Thr His Tyr Lys Thr Cys 10 20 25 28 (2) INFORMATION FOR SEQ ID NO:16: 15 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16: 20 Gln Asp Leu Ala Val Cys Asp Val Cys Asn Arg Lys Phe Arg His 10 Lys Asp Tyr Leu Arg Asp His Gln Lys Thr His 25 20 25 26 (2) INFORMATION FOR SEQ ID NO:17: (i) SEQUENCE CHARACTERISTICS: 30 (A) LENGTH: 28 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17: 35 Thr Gly Lys Tyr Pro Phe IIe Cys Ser Glu Cys Gly Lys Ser Phe 10 15 1 5 40 Met Asp Lys Arg Tyr Leu Lys Ile His Ser Asn Val His 28 20 25 (2) INFORMATION FOR SEQ ID NO:18: 45 . (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear

| | (XI) SEQUENCE DESCRIPTION: SEQ ID NO:18: |
|----|--|
| 5 | Thr Gly Glu Lys Pro Tyr Thr Cys Thr Val Cys Gly Lys Lys Phe 1 5 10 15 |
| 5 | lle Asp Arg Ser Ser Val Val Lys His Ser Arg Thr His 20 25 28 |
| 10 | (2) INFORMATION FOR SEQ ID NO:19: |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear |
| 15 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19: |
| 20 | Arg Lys Lys Phe Pro His Ile Cys Gly Glu Cys Gly Lys Gly Phe 1 5 10 15 |
| | Arg His Pro Ser Ala Leu Lys Lys His Ile Arg Val His 20 25 28 |
| 25 | (2) INFORMATION FOR SEQ ID NO:20: |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear |
| 30 | (xi) SEQUENCE, DESCRIPTION: SEQ ID NO:20: |
| 35 | Ser Glu Glu Lys Pro Phe Glu Cys Glu Glu Cys Gly Lys Lys Phe 1 5 10 15 |
| | Arg Thr Ala Arg His Leu Val Lys His Gln Arg Ile His 20 25 28 |
| 40 | (2) INFORMATION FOR SEQ ID NO:21: |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21: |
| | Pro Asn Glu Gln Met Ala Gln Cys Pro lle Cys Gln Gln Phe Tyr |

10 15 5 1 Pro Leu Lys Ala Leu Glu Lys Thr His Leu Asp Glu Cys 25 28 5 (2) INFORMATION FOR SEQ ID NO:22: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 amino acids (B) TYPE: amino acid 10 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22: Pro Asp Asp Gly Leu Val Ala Cys Pro lle Cys Leu Thr Arg Met 15 10 Lys Glu Gln Gln Val Asp Arg His Leu Asp Thr Ser Cys 25 20 (2) INFORMATION FOR SEQ ID NO:23: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 bases 25 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23: 30 **CCTTGTGCCT GCAGAGAGAA G 21** 35 (2) INFORMATION FOR SEQ ID NO:24: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases (B) TYPE: nucleic acid 40 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 45 CTAGGTTAAC TTTCGGTGCT CCCCAGCAGG GTCTC 35

| | (2) INFORMATION FOR SEQ ID NO:25: |
|----|---|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: |
| | CTAGGTTAAC TGGAGAAGGG GACCTGCTCG TCCTT 35 |
| 15 | |
| | (2) INFORMATION FOR SEQ ID NO:26: |
| 20 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 35 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26: |
| | CTAGGTTAAC TGCTGGCTTG GGAGGAGCAC TGTGA 35 |
| 30 | • |
| | (2) INFORMATION FOR SEQ ID NO:27: |
| 35 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 35 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27: |
| 45 | CTAGGTTAAC TGCTCCCGGT GCTGGCCCGG GCCTC 35 |
| | (2) INFORMATION FOR SEQ ID NO:28: |

| 5 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 34 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear |
|----|---|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28: |
| 10 | CTAGGTTAAC TGCACTGGCC GAGCTCTCCA GGGA 34 |
| 15 | (2) INFORMATION FOR SEQ ID NO:29: |
| 20 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 15 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29: |
| 25 | GTGATGAGAA TTCAT 15 |
| 30 | (2) INFORMATION FOR SEQ ID NO:30: |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single |
| 35 | (D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: |
| 40 | CGATGAATTC TCATCACTGC A 21 |
| 45 | (2) INFORMATION FOR SEQ ID NO:31: |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 bases (B) TYPE: nucleic acid |

| | (D) TOPOLOGY: linear |
|----|---|
| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31: |
| | GATCGGATCC AAAAAGAAGC CCTTGTGCCT GCA 33 |
| 10 | (2) INFORMATION FOR SEQ ID NO:32: |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32: |
| | GCCTGGTTAA CTGGGC 16 |
| 25 | (2) INFORMATION FOR SEQ ID NO:33: |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: |
| | GCNCCNATGG CNYTNGARC 19 |
| 40 | (2) INFORMATION FOR SEQ ID NO:34: |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single |

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34: |
|----|---|
| 5 | GCNCCNATGG CNYTNGARA 19 |
| | (2) INFORMATION FOR SEQ ID NO:35: |
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| 15 | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35: |
| 20 | GCNCCNATGG CNYTNGARG 19 |
| | (2) INFORMATION FOR SEQ ID NO:36: |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single |
| 30 | (D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36: |
| 35 | GYTCNARNGC CATNGGNGC 19 |
| | (2) INFORMATION FOR SEQ ID NO:37: |
| 40 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| 45 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37: |

TYTCNARNGC CATNGGNGC 19

(2) INFORMATION FOR SEQ ID NO:38:

| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
|-----|---|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38: |
| 15 | CYTCNARNGC CATNGGNGC 19 |
| 20 | (2) INFORMATION FOR SEQ ID NO:39: |
| 25 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39: |
| 30 | AARCAYGCNT AYGTNAA 17 |
| 3,5 | (2) INFORMATION FOR SEQ ID NO:40: |
| 40 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: |
| 45 | TTNACRTANG CRTGYTT 17 |

| 5 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 7 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear |
|-----|---|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41: |
| 10 | Pro Gly Ser Asn Leu Gly Ser 1 5 7 |
| | (2) INFORMATION FOR SEQ ID NO:42: |
| 15 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 8 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42: |
| | Lys Asp Asp Thr Met Phe Leu Lys 1 5 8 |
| 25 | (2) INFORMATION FOR SEQ ID NO:43: |
| 30 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 7 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43: |
| 35 | Pro Gly Ser Asn Leu Gly Ser 1 5 7 |
| | (2) INFORMATION FOR SEQ ID NO:44: |
| 40 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 8 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear |
| 4 = | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44: |
| 45 | Lys Asp Asp Thr Met Phe Leu Lys |

(2) INFORMATION FOR SEQ ID NO:41:

| | (2) INFORMATION FOR SEQ ID NO:45: | |
|------------|---|---|
| 5 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45: | |
| | TCGATCGTCG ACCAAAAAGA AGCCCTCCTG CCTACAA 37 | |
| 15 | (2) INFORMATION FOR SEQ ID NO:46: | |
| 20 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear | |
| 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46: | • |
| | CTAGAGATCT CAGGGGTCAG GCCACTTT 28 | |
| 30 | (2) INFORMATION FOR SEQ ID NO:47: | |
| 3 5 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 41 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear | |
| 40 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47: | |
| | CTAGAGATCT GTTAACTTTC GGTGCTCCCC AGCAGGGTCT C 41 | |
| 45 | (2) INFORMATION FOR SEQ ID NO:48: | |
| | (i) SEQUENCE CHARACTERISTICS: | |

| - | (A) LENGTH: 41 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear |
|----|---|
| 5 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48: |
| 10 | CTAGAGATCT GTTAACTGGA GAAGGGGACC TGCTCGTCCT T 41 |
| | (2) INFORMATION FOR SEQ ID NO:49: |
| 15 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 41 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear |
| 20 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49: |
| 25 | CTAGAGATCT GTTAACTGCT GGCTTGGGAG GAGCACTGTG A 41 |
| | (2) INFORMATION FOR SEQ ID NO:50: |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50: |
| 40 | TCGATCGTCG ACCAAAAGA AGCCCTCCTG CCTACAA 37 |
| | (2) INFORMATION FOR SEQ ID NO:51: |
| 45 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 bases (B) TYPE: nucleic acid |

(C) STRANDEDNESS: single

| | (D) TOPOLOGY: linear |
|-----------|---|
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51: |
| 5 | CTAGAGATCT CAGGGGTCAG GCCACTTT 28 |
| 10 | (2) INFORMATION FOR SEQ ID NO:52: |
| 15 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52: |
| 20 | TCGATCGTCG ACCGCCTCCA GCTCAGCCCC TGAT 34 |
| 25 | (2) INFORMATION FOR SEQ ID NO:53: |
| 30 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53: |
| 35 | GATCGGATCC GGAGACACAG ATTCCAGCCC C 31 |
| 40 | (2) INFORMATION FOR SEQ ID NO:54: |
| 45 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 35 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54: |

GATCGAATTC TTAACTCTTC GGTGCTCCCC AGCAG 35

5 (2) INFORMATION FOR SEQ ID NO:55: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases 10 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55: 15 GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30 20 (2) INFORMATION FOR SEQ ID NO:56: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 bases 25 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56: 30 **CCTGGCTGGC CTAATGT 17** 35 (2) INFORMATION FOR SEQ ID NO:57: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 bases 40 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57: 45

PA01484Fgd/am

GATCGACTCG AGATGCCCAA GAAGAAGCGG AAGGTGGCTG CAGCCAGTGT 50

GACTTCCCCT 60

| 5 | (2) INFORMATION FOR SEQ ID NO:58: |
|------------|---|
| 10 | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58: |
| 15 | CTCTGGCGAA GAAGTCC 17 |
| 20 | (2) INFORMATION FOR SEQ ID NO:59: |
| 25 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 31 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: |
| 30 | GATCGGATCC GCCTCCAGCT CAGCCCCTGA T 3 |
| 3,5 | (2) INFORMATION FOR SEQ ID NO:60: |
| 4 0 | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 31 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60: |
| 45 | GATCGGATCC AGCCAGCAGC TTCTCCTTCA C 3 |

| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61: GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30 (2) INFORMATION FOR SEQ ID NO:62: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: GATCGGATCC GCTCAGGCTC TTTTGGGGCA 30 | | (2) INFORMATION FOR SEQ ID NO:61: |
|---|----|--|
| GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30 (2) INFORMATION FOR SEQ ID NO:62: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: | 5 | (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single |
| (2) INFORMATION FOR SEQ ID NO:62: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: | 10 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61: |
| (2) INFORMATION FOR SEQ ID NO:62: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: | | GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30 |
| (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: | 15 | (2) INFORMATION FOR SEQ ID NO:62: |
| 25 | 20 | (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single |
| GATCGGATCC GCTCAGGCTC TTTTGGGGCA 30 | 25 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: |
| | | GATCGGATCC GCTCAGGCTC TTTTGGGGCA 30 |